

# Package ‘CoreGx’

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**Type** Package

**Title** Classes and Functions to Serve as the Basis for Other 'Gx' Packages

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**Description** A collection of functions and classes which serve as the foundation for our lab's suite of R packages, such as 'PharmacoGx' and 'RadioGx'. This package was created to abstract shared functionality from other lab package releases to increase ease of maintainability and reduce code repetition in current and future 'Gx' suite programs. Major features include a 'CoreSet' class, from which 'RadioSet' and 'PharmacoSet' are derived, along with get and set methods for each respective slot. Additional functions related to fitting and plotting dose response curves, quantifying statistical correlation and calculating area under the curve (AUC) or survival fraction (SF) are included. For more details please see the included documentation, as well as:

Smirnov, P., Safikhani, Z., El-Hachem, N., Wang, D., She, A., Olsen, C., Freeman, M., Selby, H., Gendoo, D., Grossman, P., Beck, A., Aerts, H., Lupien, M., Goldenberg, A. (2015) <doi:10.1093/bioinformatics/btv723>. Manem, V., Labie, M., Smirnov, P., Kofia, V., Freeman, M., Koritzinsky, M., Abazeed, M., Haibe-Kains, B., Bratman, S. (2018) <doi:10.1101/449793>.

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'cosinePerm.R' 'datasets.R' 'globals.R' 'gwc.R' 'matthewCor.R'  
 'methods-\$.R' 'methods-[.R' 'methods-[[.R'  
 'methods-annotation.R' 'methods-assay.R' 'methods-assayNames.R'  
 'methods-assays.R' 'methods-buildLongTable.R'  
 'methods-cellInfo.R' 'methods-cellNames.R' 'methods-coerce.R'  
 'methods-colData.R' 'methods-curation.R'  
 'methods-datasetType.R' 'methods-dateCreated.R' 'methods-dim.R'  
 'methods-dimnames.R' 'methods-drugSensitivitySig.R'  
 'methods-fNames-methods.R' 'methods-featureInfo.R'  
 'methods-getIntern.R' 'methods-intersect.R'  
 'methods-mDataNames.R' 'methods-metadata.R'  
 'methods-molecularProfiles.R' 'methods-molecularProfilesSlot.R'  
 'methods-name.R' 'methods-pertNumber.R' 'methods-phenoInfo.R'  
 'methods-reindex.R' 'methods-rowData.R' 'methods-sensNumber.R'  
 'methods-sensitivityInfo.R' 'methods-sensitivityMeasures.R'  
 'methods-sensitivityProfiles.R'  
 'methods-sensitivityRaw-methods.R'  
 'methods-sensitivitySlot-methods.R' 'methods-subset.R'  
 'methods-subsetTo.R' 'utilities.R'

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---

*Convenience function for converting R code to a call*

---

### Description

This is used to pass through unevaluated R expressions into subset and '[', where they will be evaluated in the correct context.

### Usage

```
.(...)
```

### Arguments

... [*'parilist'*] One or more R expressions to convert to calls.

### Value

'call' An R call object containing the quoted expression.

### Examples

```
.(cell_line1 == 'A2058')
```

---

amcc

*Calculate an Adaptive Matthews Correlation Coefficient*

---

### Description

This function calculates an Adaptive Matthews Correlation Coefficient (AMCC) for two vectors of values of the same length. It assumes the entries in the two vectors are paired. The Adaptive Matthews Correlation Coefficient for two vectors of values is defined as the Maximum Matthews Coefficient over all possible binary splits of the ranks of the two vectors. In this way, it calculates the best possible agreement of a binary classifier on the two vectors of data. If the AMCC is low, then it is impossible to find any binary classification of the two vectors with a high degree of concordance.

### Usage

```
amcc(x, y, step.prct = 0, min.cat = 3, nperm = 1000, nthread = 1, ...)
```

**Arguments**

x, y	Two paired vectors of values. Could be replicates of observations for the same experiments for example.
step.prc	Instead of testing all possible splits of the data, it is possible to test steps of a percentage size of the total number of ranks in x/y. If this variable is 0, function defaults to testing all possible splits.
min.cat	The minimum number of members per category. Classifications with less members fitting into both categories will not be considered.
nperm	The number of perumutation to use for estimating significance. If 0, then no p-value is calculated.
nthread	Number of threads to parallize over. Both the AMCC calculation and the permutation testing is done in parallel.
...	Additional arguments

**Value**

Returns a list with two elements. \$amcc contains the highest 'mcc' value over all the splits, the p value, as well as the rank at which the split was done.

**Examples**

```
x <- c(1,2,3,4,5,6,7)
y <- c(1,3,5,4,2,7,6)
amcc(x,y, min.cat=2)
```

annotation<- ,CoreSet,list-method  
*annotation<- Slot Setter*

**Description**

annotation<- Slot Setter

**Usage**

```
## S4 replacement method for signature 'CoreSet,list'
annotation(object) <- value
```

**Arguments**

object	A RadioSet
value	A list of annotations to add to the annotatiosn slot of an rSet

**Value**

A copy of the CoreSet with the updated annotation slot

**Functions**

- annotation<- ,CoreSet,list-method: Update the annotation slot of a tSet

**Examples**

```
annotation(clevelandSmall_cSet) <- annotation(clevelandSmall_cSet)
```

---

as *LongTable to data.table conversion*

---

**Description**

Coerce a LongTable into a 'data.table'.

Currently only supports coercing to data.table or data.frame

Coerce a data.table with the proper configuration attributes back to a LongTable

**Arguments**

to	['character'] Class name to coerce to, currently only 'data.table' and 'data.frame' are supported
from	A ['data.table'] with the 'LongTable.config' attribute, containing three lists named assayCols, rowDataCols and colDataCols. This attribute is automatically created when coercing from a 'LongTable' to a 'data.table'.

**Value**

A ['data.table'] with the data from a LongTable.

['data.table'] containing the data from the LongTable, with the 'LongTable.config' attribute containing the metadata needed to reverse the coercing operation.

['LongTable'] object configured with the LongTable.config

**Examples**

```
as(merckLongTable, 'data.table')

dataTable <- as(merckLongTable, 'data.table')
print(attr(dataTable, 'LongTable.config')) # Method doesn't work without this
as(dataTable, 'LongTable')
```

---

as.data.frame.LongTable  
*Coerce a LongTable to a data.frame*

---

**Description**

S3 version of coerce method for convenience.

**Usage**

```
## S3 method for class 'LongTable'
as.data.frame(x, row.names, optional = TRUE, ...)
```

**Arguments**

x	[‘LongTable‘] to coerce to ‘data.frame‘.
row.names	An optional [‘character‘] vector of rownames. We do not recommend using this parameter, it is included for S3 method consistency with ‘as.data.frame‘.
optional	[‘logical‘] Is it optional for row and column names to be valid R names? If FALSE will use the make.names function to ensure the row and column names are valid R names. Defaults to TRUE.
...	Does nothing.

**Value**

‘data.frame‘ containing the data from the LongTable, with the ‘LongTable.config’ attribute containing the metadata needed to reverse the coercion operation.

**Examples**

```
as(merckLongTable, 'data.frame')
```

---

as.data.table.LongTable

*Coerce a LongTable into a ‘data.table‘*

---

**Description**

S3 version of coerce method for convenience.

**Usage**

```
## S3 method for class 'LongTable'  
as.data.table(x)
```

**Arguments**

x	[‘LongTable‘] to coerce to a ‘data.table‘
---	---

**Value**

A [‘data.table‘] containing the data from the LongTable, as well as the ‘LongTable.config’ attribute which contains the data needed to reverse the coercion.

---

<code>as.long.table</code>	<i>Coerce from data.table to LongTable</i>
----------------------------	--

---

**Description**

Coerce a `data.table` with the proper configuration attributes back to a `LongTable`

**Usage**

```
as.long.table(x)
```

**Arguments**

<code>x</code>	A [ <code>'data.frame'</code> ] with the <code>'LongTable.config'</code> attribute, containing three lists named <code>assayCols</code> , <code>rowDataCols</code> and <code>colDataCols</code> . This attribute is automatically created when coercing from a <code>LongTable</code> to a <code>data.table</code> .
----------------	--

**Value**

`'LongTable'` object configured with the `LongTable.config`

**Examples**

```
dataTable <- as(merckLongTable, 'data.table')
print(attr(dataTable, 'LongTable.config')) # Method doesn't work without this
as.long.table(dataTable)
```

---

<code>assayCols</code>	<i>Generic to access the assay columns of a rectangular object.</i>
------------------------	---

---

**Description**

Generic to access the assay columns of a rectangular object.

**Usage**

```
assayCols(object, ...)
```

**Arguments**

<code>object</code>	[ <code>'S4'</code> ] An object to get assay ids from.
<code>...</code>	Allow new arguments to this generic.

**Value**

Depends on the implemented method.

**Examples**

```
print("Generics shouldn't need examples?")
```



---

buildLongTable	<i>Build a LongTable object</i>
----------------	---------------------------------

---

**Description**

Build a LongTable object

**Usage**

```
buildLongTable(from, ...)
```

**Arguments**

from	What to build the LongTable from?
...	['pairlist'] Allow definition of new parameters for implementations of this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

buildLongTable, list-method	<i>LongTable build method from list</i>
-----------------------------	---

---

**Description**

LongTable build method from list

**Usage**

```
## S4 method for signature 'list'
buildLongTable(from, rowDataCols, colDataCols, assayCols)
```

**Arguments**

from	['list'] A list containing any combination of character file paths, data.tables and data.frames which will be used to construct the LongTable.
rowDataCols	['list'] List with two 'character' vectors, the first specifying one or more columns to be used as cell identifiers (e.g., cell-line name columns) and the second containing any additional metadata columns related to the cell identifiers.
colDataCols	['list'] List with two 'character' vectors, the first specifying one or more columns to be used as column identifiers (e.g., drug name columns) and the second containing any additional metadata columns related to the column identifiers.
assayCols	['list'] A named list of character vectors specifying how to parse assay columns into a list of 'data.table's. Each list data.table will be named for the name of corresponding list item and contain the columns specified in the character vector of column names in each list item.

**Value**

A [`'LongTable'`] object constructed with the data in `'from'`.

**Functions**

- `buildLongTable`, `list-method`: a `LongTable` object from a list containing file paths, `data.frames` and `data.tables`.

**Examples**

```
assayList <- assays(merckLongTable, withDimnames=TRUE)
rowDataCols <- list(rowIDs(merckLongTable))
colDataCols <- list(colIDs(merckLongTable), colMeta(merckLongTable))
assayCols <- assayCols(merckLongTable)
longTable <- buildLongTable(from=assayList, rowDataCols, colDataCols, assayCols)
```

---

cellInfo

*cellInfo Getter*

---

**Description**

Get cell line information from a `PharmacoSet` object

**Usage**

```
cellInfo(object, ...)
```

**Arguments**

<code>object</code>	The <code>CoreSet</code> to retrieve cell info from
<code>...</code>	<code>list</code> Fall through arguments to allow generic to be defined with different parameters

**Value**

a `data.frame` with the cell annotations

**Examples**

```
cellInf <- cellInfo(clevelandSmall_cSet)
```

---

cellInfo<-	<i>cellInfo&lt;- Generic</i>
------------	------------------------------

---

**Description**

Generic for cellInfo replace method

**Usage**

```
cellInfo(object) <- value
```

**Arguments**

object	The CoreSet to replace cell info in
value	A data.frame with the new cell annotations

**Value**

Updated CoreSet

**Examples**

```
cellInfo(clevelandSmall_cSet) <- cellInfo(clevelandSmall_cSet)
```

---

cellNames	<i>cellNames Generic</i>
-----------	--------------------------

---

**Description**

A generic for the cellNames method

**Usage**

```
cellNames(object, ...)
```

**Arguments**

object	The CoreSet to return cell names from
...	Fallthrough arguments for defining new methods

**Value**

A vector of the cell names used in the CoreSet

**Examples**

```
cellNames(clevelandSmall_cSet)
```

---

cellNames<-                    *cellNames<- Generic*

---

**Description**

A generic for the cellNames replacement method

**Usage**

```
cellNames(object, ...) <- value
```

**Arguments**

object	The CoreSet to update
...	Fallthrough arguments for defining new methods
value	A character vector of the new cell names

**Value**

Updated CoreSet

**Examples**

```
cellNames(clevelandSmall_cSet) <- cellNames(clevelandSmall_cSet)
```

---

checkCsetStructure            *A function to verify the structure of a CoreSet*

---

**Description**

This function checks the structure of a PharamcoSet, ensuring that the correct annotations are in place and all the required slots are filled so that matching of cells and drugs can be properly done across different types of data and with other studies.

**Usage**

```
checkCsetStructure(cSet, plotDist = FALSE, result.dir = ".")
```

**Arguments**

cSet	A CoreSet to be verified
plotDist	Should the function also plot the distribution of molecular data?
result.dir	The path to the directory for saving the plots as a string

**Value**

Prints out messages whenever describing the errors found in the structure of the cSet object passed in.

**Examples**

```
checkCsetStructure(clevelandSmall_cSet)
```

---

```
clevelandSmall_cSet  Cleveland_mut RadioSet subsetted and cast as CoreSet
```

---

**Description**

This dataset is just a dummy object derived from the Cleveland\_mut RadioSet in the RadioGx R package. It's contents should not be interpreted and it is only present to test the functions in this package and provide examples

**Usage**

```
data(clevelandSmall_cSet)
```

**Format**

CoreSet object

**References**

Lamb et al. The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease. Science, 2006.

---

```
colIDs  Generic to access the row identifiers for an object.
```

---

**Description**

Generic to access the row identifiers for an object.

**Usage**

```
colIDs(object, ...)
```

**Arguments**

object	[‘S4’] An object to get column id columns from.
...	Allow new arguments to this generic

**Value**

Depends on the implemented method.

**Examples**

```
print("Generics shouldn't need examples?")
```

---

colMeta	<i>Generic to access the column identifiers for a rectangular object.</i>
---------	---

---

**Description**

Generic to access the column identifiers for a rectangular object.

**Usage**

```
colMeta(object, ...)
```

**Arguments**

object	[‘S4’] An object to get column metadata columns from.
...	Allow new arguments to this generic

**Value**

Depends on impemented method.

**Examples**

```
print("Generics shouldn't need examples?")
```

---

connectivityScore	<i>Function computing connectivity scores between two signatures</i>
-------------------	--

---

**Description**

A function for finding the connectivity between two signatures, using either the GSEA method based on the KS statistic, or the gwc method based on a weighted spearman statistic. The GSEA analysis is implemented in the piano package.

**Usage**

```
connectivityScore(
  x,
  y,
  method = c("fgsea", "gwc"),
  nperm = 10000,
  nthread = 1,
  gwc.method = c("spearman", "pearson"),
  ...
)
```

**Arguments**

x	A matrix with the first gene signature. In the case of GSEA the vector of values per gene for GSEA in which we are looking for an enrichment. In the case of gwc, this should be a matrix, with the per gene responses in the first column, and the significance values in the second.
y	A matrix with the second signature. In the case of GSEA, this is the vector of up and down regulated genes we are looking for in our signature, with the direction being determined from the sign. In the case of gwc, this should be a matrix of identical size to x, once again with the per gene responses in the first column, and their significance in the second.
method	character string identifying which method to use, out of 'fgsea' and 'gwc'
nperm	numeric, how many permutations should be done to determine significance through permutation testing? The minimum is 100, default is 1e4.
nthread	numeric, how many cores to run parallel processing on.
gwc.method	character, should gwc use a weighted spearman or pearson statistic?
...	Additional arguments passed down to gsea and gwc functions

**Value**

numeric a numeric vector with the score and the p-value associated with it

**References**

F. Pozzi, T. Di Matteo, T. Aste, 'Exponential smoothing weighted correlations', The European Physical Journal B, Vol. 85, No 6, 2012. DOI: 10.1140/epjb/e2012-20697-x

Varemo, L., Nielsen, J. and Nookaew, I. (2013) Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. Nucleic Acids Research. 41 (8), 4378-4391. doi: 10.1093/nar/gkt111

**Examples**

```
xValue <- c(1,5,23,4,8,9,2,19,11,12,13)
xSig <- c(0.01, 0.001, .97, 0.01,0.01,0.28,0.7,0.01,0.01,0.01,0.01)
yValue <- c(1,5,10,4,8,19,22,19,11,12,13)
ySig <- c(0.01, 0.001, .97,0.01, 0.01,0.78,0.9,0.01,0.01,0.01,0.01)
xx <- cbind(xValue, xSig)
yy <- cbind(yValue, ySig)
rownames(xx) <- rownames(yy) <- c('1','2','3','4','5','6','7','8','9','10','11')
data.cor <- connectivityScore(xx,yy,method='gwc', gwc.method='spearman', nperm=300)
```

---

CoreSet

*CoreSet constructor*


---

**Description**

A constructor that simplifies the process of creating CoreSets, as well as creates empty objects for data not provided to the constructor. Only objects returned by this constructor are expected to work with the CoreSet methods.

**Usage**

```

CoreSet(
  name,
  molecularProfiles = list(),
  cell = data.frame(),
  sensitivityInfo = data.frame(),
  sensitivityRaw = array(dim = c(0, 0, 0)),
  sensitivityProfiles = matrix(),
  sensitivityN = matrix(nrow = 0, ncol = 0),
  perturbationN = array(NA, dim = c(0, 0, 0)),
  curationCell = data.frame(),
  curationTissue = data.frame(),
  datasetType = c("sensitivity", "perturbation", "both"),
  verify = TRUE
)

```

**Arguments**

name	A character string detailing the name of the dataset
molecularProfiles	A list of SummarizedExperiment objects containing molecular profiles for each molecular data type.
cell	A data.frame containing the annotations for all the cell lines profiled in the data set, across all data types
sensitivityInfo	A data.frame containing the information for the sensitivity experiments
sensitivityRaw	A 3 Dimensional array containing the raw drug dose response data for the sensitivity experiments
sensitivityProfiles	data.frame containing drug sensitivity profile statistics such as IC50 and AUC
sensitivityN, perturbationN	A data.frame summarizing the available sensitivity/perturbation data
curationCell, curationTissue	A data.frame mapping the names for cells and tissues used in the data set to universal identifiers used between different CoreSet objects
datasetType	A character string of 'sensitivity', 'preturbation', or both detailing what type of data can be found in the CoreSet, for proper processing of the data
verify	boolean Should the function verify the CoreSet and print out any errors it finds after construction?

**Value**

An object of class CoreSet



---

CoreSet-class	<i>A Superclass to Contain Data for Genetic Profiling and Viability Screens of Cancer Cell Lines</i>
---------------	--

---

### Description

The CoreSet (CSet) class was developed as a superclass for pSets in the PharmacGx and RadioGx packages to contain the data generated in screens of cancer cell lines for their genetic profile and sensitivities to therapy (Pharmacological or Radiation). This class is meant to be a superclass which is contained within the PharmacSet (pSet) and RadioSet (RSet) objects exported by PharmacGx and RadioGx. The format of the data is similar for both pSets and rSets, allowing much of the code to be abstracted into the CoreSet super-class. However, the models involved with quantifying cellular response to Pharmacological and Radiation therapy are widely different, and extension of the cSet class allows the packages to apply the correct model for the given data.

Generic for sensitivityInfo method

A generic for the sensitivityInfo replacement method

### Usage

```
## S4 method for signature 'CoreSet'
annotation(object)

## S4 method for signature 'CoreSet'
cellInfo(object)

## S4 replacement method for signature 'CoreSet,data.frame'
cellInfo(object) <- value

## S4 method for signature 'CoreSet'
cellNames(object)

## S4 replacement method for signature 'CoreSet,character'
cellNames(object) <- value

## S4 method for signature 'CoreSet'
curation(object)

## S4 replacement method for signature 'CoreSet,list'
curation(object) <- value

## S4 method for signature 'CoreSet'
datasetType(object)

## S4 replacement method for signature 'CoreSet'
datasetType(object) <- value

## S4 method for signature 'CoreSet'
dateCreated(object)

## S4 replacement method for signature 'CoreSet'
```

```
dateCreated(object) <- value

## S4 method for signature 'CoreSet'
fNames(object, mDataType)

## S4 replacement method for signature 'CoreSet,character,character'
fNames(object, mDataType) <- value

## S4 method for signature 'CoreSet'
featureInfo(object, mDataType)

## S4 replacement method for signature 'CoreSet,character,data.frame'
featureInfo(object, mDataType) <- value

## S4 replacement method for signature 'CoreSet,character,DataFrame'
featureInfo(object, mDataType) <- value

## S4 method for signature 'CoreSet'
mDataNames(object)

## S4 replacement method for signature 'CoreSet'
mDataNames(object) <- value

## S4 method for signature 'CoreSet'
molecularProfiles(object, mDataType, assay)

## S4 replacement method for signature 'CoreSet,character,character,matrix'
molecularProfiles(object, mDataType, assay) <- value

## S4 replacement method for signature 'CoreSet,character,missing,matrix'
molecularProfiles(object, mDataType, assay) <- value

## S4 method for signature 'CoreSet'
molecularProfilesSlot(object)

## S4 replacement method for signature 'CoreSet,list'
molecularProfilesSlot(object) <- value

## S4 method for signature 'CoreSet'
name(object)

## S4 replacement method for signature 'CoreSet'
name(object) <- value

## S4 method for signature 'CoreSet'
pertNumber(object)

## S4 replacement method for signature 'CoreSet,array'
pertNumber(object) <- value

## S4 method for signature 'CoreSet'
phenoInfo(object, mDataType)
```

```

## S4 replacement method for signature 'CoreSet,character,data.frame'
phenoInfo(object, mDataType) <- value

## S4 replacement method for signature 'CoreSet,character,DataFrame'
phenoInfo(object, mDataType) <- value

## S4 method for signature 'CoreSet'
sensNumber(object)

## S4 replacement method for signature 'CoreSet,matrix'
sensNumber(object) <- value

## S4 method for signature 'CoreSet'
sensitivityInfo(object)

## S4 replacement method for signature 'CoreSet,data.frame'
sensitivityInfo(object) <- value

## S4 method for signature 'CoreSet'
sensitivityMeasures(object)

## S4 replacement method for signature 'CoreSet,character'
sensitivityMeasures(object) <- value

## S4 method for signature 'CoreSet'
sensitivityProfiles(object)

## S4 replacement method for signature 'CoreSet,data.frame'
sensitivityProfiles(object) <- value

## S4 replacement method for signature 'CoreSet,matrix'
sensitivityProfiles(object) <- value

## S4 method for signature 'CoreSet'
sensitivityRaw(object)

## S4 replacement method for signature 'CoreSet,array'
sensitivityRaw(object) <- value

## S4 method for signature 'CoreSet'
sensitivitySlot(object)

## S4 replacement method for signature 'CoreSet,list'
sensitivitySlot(object) <- value

```

### Arguments

object	An ['CoreSet'] to extract the raw sensitivity data from.
value	A 3D ['array'] containing the raw dose and viability measurements to update the object with.
mDataType	character The type of molecular data

**assay** character Name of the desired assay; if excluded defaults to first assay in the SummarizedExperiment for the given mDataType. Use assayNames(molecularProfiles(object, mDataType)) to check which assays are available for a given molecular datatype.

### Value

An object of the CoreSet class

A list of named annotation

A list of unique cell and tissue identifiers to check validity of a cSet

A copy of the RadioSet with the updated curation slot

a data.frame with the experiment info if dimension is excluded, otherwise a 'data.table' with annotations for the cells or drugs dimension of the LongTable.

Updated CoreSet

A ['character'] vector of all the available sensitivity measures.

A update CoreSet object with the new sensitivity measures

a ['data.frame'] with sensitivity profile summaries for CoreSet

Updated CoreSet

A ['array'] containing the raw sensitivity data as experiment by dose level by metric.

A 3D ['array'] containing the raw sensitivity data as experiment by dose level by metric.

### Methods (by generic)

- **annotation**: Retrieve the annotations slot form an rSet
- **cellInfo**: Returns the annotations for all the cell lines tested on in the CoreSet
- **cellInfo<-**: Update the cell line annotations
- **cellNames**: Return the cell names used in the dataset
- **cellNames<-**: Update the cell names used in the dataset
- **curation**: Retrieve the curation slot form a cSet
- **curation<-**: Update the curation slot of a cSet
- **datasetType**: Update the dataset type of an rSet and return a copy of the updated object
- **datasetType<-**: Update the dataset type of an rSet and return a copy of the updated object
- **dateCreated**: Return the date the CoreSet was created
- **dateCreated<-**: Update the date a cSet was created
- **fNames**: Return the feature names used in the dataset
- **fNames<-**: Update the feature names used in a molecular profile
- **featureInfo**: Return the feature info for the given molecular data
- **featureInfo<-**: Replace the gene info for the molecular data
- **featureInfo<-**: Replace the gene info for the molecular data
- **mDataNames**: Return the molecular data types available in a cSet object
- **mDataNames<-**: Return the molecular data types available in a cSet object
- **molecularProfiles**: Return the given type of molecular data from the CoreSet
- **molecularProfiles<-**: Update the given type of molecular data from the CoreSet
- **molecularProfiles<-**: Update the given type of molecular data from the CoreSet

- `molecularProfilesSlot`: Return a list containing all `molecularProfiles` in the `cSet`
- `molecularProfilesSlot<-`: Update the contents of the `molecularProfiles` slot in a `CoreSet` and returns an update copy
- `name`: Return the name of the `CoreSet`
- `name<-`: Return the name of the `CoreSet`
- `pertNumber`: Return the summary of available perturbation experiments
- `pertNumber<-`: Update the summary of available perturbation experiments
- `phenoInfo`: Return the experiment info from the given type of molecular data in `CoreSet`
- `phenoInfo<-`: Update the given type of molecular data experiment info in the `CoreSet`
- `phenoInfo<-`: Update the given type of molecular data experiment info in the `CoreSet`
- `sensNumber`: Return the summary of available sensitivity experiments
- `sensNumber<-`: Update the summary of available sensitivity experiments
- `sensitivityInfo`: Return the drug dose sensitivity experiment info
- `sensitivityInfo<-`: Update the sensitivity experiment info
- `sensitivityMeasures`: Returns the available sensitivity profile summaries, for example, whether there are IC50 values available
- `sensitivityMeasures<-`: Updates the sensitivity measures in a 'CoreSet' object and returns the updated object
- `sensitivityProfiles`: Return the sensitivity profile summaries from the sensitivity slot.
- `sensitivityProfiles<-`: Update the sensitivity profile summaries the sensitivity slot.
- `sensitivityProfiles<-`: Update the phenotypic data for the drug dose sensitivity
- `sensitivityRaw`: Get the raw dose and viability data from a `CoreSet` object.
- `sensitivityRaw<-`: Set the raw dose and viability data for a `cSet` and return and updated copy
- `sensitivitySlot`: Retrieve the contents of the sensitivity slot
- `sensitivitySlot<-`: Set the raw dose and viability data for a `cSet` and return and updated copy

## Slots

- `annotation` A list of annotation data about the `CoreSet`, including the `$name` and the session information for how the object was created, detailing the exact versions of R and all the packages used
- `molecularProfiles` A list containing `SummarizedExperiments` type object for holding data for RNA, DNA, SNP and Copy Number Variation measurements respectively, with associated `rowData` and `colData` containing the row and column metadata
- `cell` A `data.frame` containing the annotations for all the cell lines profiled in the data set, across all data types
- `sensitivity` A list containing all the data for the sensitivity experiments, including `$info`, a `data.frame` containing the experimental info, `$raw` a 3D array containing raw data, `$profiles`, a `data.frame` containing sensitivity profiles statistics, and `$n`, a `data.frame` detailing the number of experiments for each cell-drug/radiationInfo pair
- `perturbation` A list containing `$n`, a `data.frame` summarizing the available perturbation data,
- `curation` A list containing mappings for cell, tissue names used in the data set to universal identifiers used between different `CoreSet` objects
- `datasetType` A character string of 'sensitivity', 'perturbation', or both detailing what type of data can be found in the `CoreSet`, for proper processing of the data

**Examples**

```
annotation(clevelandSmall_cSet)

data(clevelandSmall_cSet)
curation(clevelandSmall_cSet)

data(clevelandSmall_cSet)
curation(clevelandSmall_cSet) <- curation(clevelandSmall_cSet)

data(clevelandSmall_cSet)
sensitivityInfo(clevelandSmall_cSet)

sensitivityInfo(clevelandSmall_cSet) <- sensitivityInfo(clevelandSmall_cSet)

sensitivityMeasures(clevelandSmall_cSet)

data(clevelandSmall_cSet)
sensitivityMeasures(clevelandSmall_cSet) <- sensitivityMeasures(clevelandSmall_cSet)

sensitivityProfiles(clevelandSmall_cSet)

sensitivityProfiles(clevelandSmall_cSet) <- sensitivityProfiles(clevelandSmall_cSet)

data(clevelandSmall_cSet)
sensRaw <- sensitivityRaw(clevelandSmall_cSet)
head(sensRaw)

data(clevelandSmall_cSet)
sensitivityRaw(clevelandSmall_cSet) <- sensitivityRaw(clevelandSmall_cSet)
```

---

cosinePerm

*Cosine Permutations*

---

**Description**

Computes the cosine similarity and significance using permutation test. This function uses random numbers, to ensure reproducibility please call `set.seed()` before running the function.

**Usage**

```
cosinePerm(
  x,
  y,
  nperm = 1000,
  alternative = c("two.sided", "less", "greater"),
  include.perm = FALSE,
  nthread = 1,
  ...
)
```

**Arguments**

x	factor is the factors for the first variable
y	factor is the factors for the second variable
nperm	integer is the number of permutations to compute the null distribution of MCC estimates
alternative	string indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association. Options are 'two.sided', 'less', or 'greater'
include.perm	boolean indicates whether the estimates for the null distribution should be returned. Default set to 'FALSE'
nthread	integer is the number of threads to be used to perform the permutations in parallel
...	A list of fallthrough parameters

**Value**

A list estimate of the cosine similarity, p-value and estimates after random permutations (null distribution) in include.perm is set to 'TRUE'

**Examples**

```
x <- factor(c(1,2,1,2,1))
y <- factor(c(2,2,1,1,1))
cosinePerm(x, y)
```

---

curation

*curation Slot Getter*


---

**Description**

curation Slot Getter

**Usage**

```
curation(object, ...)
```

**Arguments**

object	A object
...	A list to allow definition of new parameters on this generic

**Value**

A list of unique cell and tissue identifiers to check validity of an rSet

**Examples**

```
data(clevelandSmall_cSet)
curation(clevelandSmall_cSet)
```

---

curation<-                    *curation<- Slot Setter*

---

**Description**

```
#' @examples data(clevelandSmall_cSet) curation(clevelandSmall_cSet) <- curation(clevelandSmall_cSet)
```

**Usage**

```
curation(object, ...) <- value
```

**Arguments**

object	A object
...	A list to allow definition of new parameters on this generic
value	A list of curations for the cell and tissues types in the rSet object

**Value**

A copy of the RadioSet with the updated curation slot

---

datasetType                    *datasetType Generic*

---

**Description**

A generic for retrieving the dataset type of an rSet object

**Usage**

```
datasetType(object, ...)
```

**Arguments**

object	A CoreSet from which to retrieve the dataset type
...	A list containing fall through arguments; this allows addition of new parameters to methods for this generic

**Value**

A character vector containing the dataset type

**Examples**

```
data(clevelandSmall_cSet)
datasetType(clevelandSmall_cSet)
```



---

datasetType<-                    *datasetType<- Replacement Generic*

---

**Description**

A generic for updating the dataset type of a RadioSet object

**Usage**

```
datasetType(object) <- value
```

**Arguments**

object	A RadioSet from which to retrieve the dataset type
value	A character vector containing the dataset type

**Value**

A character vector containing the dataset type

**Examples**

```
data(clevelandSmall_cSet)
datasetType(clevelandSmall_cSet)
```

---

dateCreated                    *dateCreated Generic*

---

**Description**

A generic for the dateCreated method

**Usage**

```
dateCreated(object, ...)
```

**Arguments**

object	A CoreSet
...	Fallthrough arguments for defining new methods

**Value**

The date the CoreSet was created

**Examples**

```
dateCreated(clevelandSmall_cSet)
```

---

dateCreated<-                    *dateCreated<- Generic*

---

**Description**

A generic for the dateCreated method

**Usage**

```
dateCreated(object, ...) <- value
```

**Arguments**

object	A CoreSet
...	Fallthrough arguements for defining new methods
value	A datet ime object to update the cSet with

**Value**

The date the CoreSet was created

**Examples**

```
dateCreated(clevelandSmall_cSet) <- date()
```

---

featureInfo                    *featureInfo Generic*

---

**Description**

Generic for featureInfo method

**Usage**

```
featureInfo(object, mDataType, ...)
```

**Arguments**

object	The CoreSet to retrieve feature annotations from
mDataType	the type of molecular data
...	Fallthrough arguements for defining new methods

**Value**

a data.frame with the feature annotations

**Examples**

```
featureInfo(clevelandSmall_cSet, "rna")
```

---

featureInfo<-	<i>featureInfo&lt;- Generic</i>
---------------	---------------------------------

---

**Description**

Generic for featureInfo replace method

**Usage**

```
featureInfo(object, mDataType) <- value
```

**Arguments**

object	The CoreSet to replace gene annotations in
mDataType	The type of molecular data to be updated
value	A data.frame with the new feature annotations

**Value**

Updated CoreSet

**Examples**

```
featureInfo(clevelandSmall_cSet, "rna") <- featureInfo(clevelandSmall_cSet, "rna")
```

---

fNames	<i>fNames Generic</i>
--------	-----------------------

---

**Description**

A generic for the fNames method

**Usage**

```
fNames(object, mDataType, ...)
```

**Arguments**

object	The CoreSet
mDataType	The molecular data type to return feature names for
...	Fallthrough arguments for defining new methods

**Value**

A character vector of the feature names

**Examples**

```
fNames(clevelandSmall_cSet, "rna")
```

---

```
fNames<-          fNames<- Generic
```

---

**Description**

A generic for the fNames replacement method

**Usage**

```
fNames(object, mDataType) <- value
```

**Arguments**

object	The CoreSet to update
mDataType	The molecular data type to update
value	A character vector of the new cell names

**Value**

Updated CoreSet

**Examples**

```
data(clevelandSmall_cSet)
fNames(clevelandSmall_cSet, "rna") <- fNames(clevelandSmall_cSet, "rna")
```

---

```
getIntern          Retrieve the symbol for the object@.intern slot
```

---

**Description**

Internal slot for storing metadata relevant to the internal operation of an S4 object.

**Usage**

```
getIntern(object, x, ...)
```

**Arguments**

object	[‘S4’] An object with an @.intern slot containing an environment.
x	[‘character’] One or more symbol names to retrieve from the object@.intern environment.
...	Allow new parameters to be defined for this generic.

**Details**

Warning: This method is intended for developer use and can be ignored by users.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

gwc	<i>GWC Score</i>
-----	------------------

---

**Description**

Calculate the gwc score between two vectors, using either a weighted spearman or pearson correlation

**Usage**

```
gwc(
  x1,
  p1,
  x2,
  p2,
  method.cor = c("pearson", "spearman"),
  nperm = 10000,
  truncate.p = 1e-16,
  ...
)
```

**Arguments**

x1	numeric vector of effect sizes (e.g., fold change or t statistics) for the first experiment
p1	numeric vector of p-values for each corresponding effect size for the first experiment
x2	numeric effect size (e.g., fold change or t statistics) for the second experiment
p2	numeric vector of p-values for each corresponding effect size for the second experiment
method.cor	character string identifying if a pearson or spearman correlation should be used
nperm	numeric how many permutations should be done to determine
truncate.p	numeric Truncation value for extremely low p-values
...	Other passed down to internal functions

**Value**

numeric a vector of two values, the correlation and associated p-value.

**Examples**

```

data(clevelandSmall_cSet)
x <- molecularProfiles(clevelandSmall_cSet, 'rna')[,1]
y <- molecularProfiles(clevelandSmall_cSet, 'rna')[,2]
x_p <- rep(0.05, times=length(x))
y_p <- rep(0.05, times=length(y))
names(x_p) <- names(x)
names(y_p) <- names(y)
gwc(x,x_p,y,y_p, nperm=100)

```

---

idCols

*Generic to access the unique id columns in an S4 object used to*


---

**Description**

Generic to access the unique id columns in an S4 object used to

**Usage**

```
idCols(object, ...)
```

**Arguments**

object	An ['S4'] object to get id columns from.
...	Allow new arguments to this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

idCols,LongTable-method

*Retrieve the unique identifier columns used for primary keys in row-Data and colData.*


---

**Description**

Retrieve the unique identifier columns used for primary keys in rowData and colData.

**Usage**

```
## S4 method for signature 'LongTable'
idCols(object)
```

**Arguments**

object            [‘LongTable’]

**Value**

‘character’ A character vector containing the unique rowIDs and colIDs in a LongTable object.

**Examples**

```
idCols(merckLongTable)
```

---

<code>is.items</code>	<i>Get the types of all items in a list</i>
-----------------------	---

---

**Description**

Get the types of all items in a list

**Usage**

```
is.items(list, ..., FUN = is)
```

**Arguments**

<code>list</code>	A [‘list’] to get the types from
<code>...</code>	[‘pairlist’] Additional arguments to FUN
<code>FUN</code>	[‘function’] or [‘character’] Either a function, or the name of a function which returns a single logical value. The default function uses ‘is’, specify the desired type in ‘...’. You can also use other type checking functions such as <code>is.character</code> , <code>is.numeric</code> , or <code>is.data.frame</code> .

**Value**

‘logical’ A vector indicating if the list item is the specified type.

**Examples**

```
list <- list(c(1,2,3), c('a','b','c'))
is.items(list, 'character')
```

---

<code>list_or_LongTable-class</code>	<i>A class union to allow multiple types in a CoreSet slot</i>
--------------------------------------	--

---

**Description**

A class union to allow multiple types in a CoreSet slot

---

LongTable

*LongTable constructor method*


---

### Description

Builds a ‘LongTable’ object from rectangular objects. The ‘rowData’ argument should contain row level metadata, while the ‘colData’ argument should contain column level metadata, for the experimental assays in the ‘assays’ list. The ‘rowIDs’ and ‘colIDs’ lists are used to configure the internal keys mapping rows or columns to rows in the assays. Each list should contain at minimum one character vector, specifying which columns in ‘rowData’ or ‘colData’ are required to uniquely identify each row. An optional second character vector can be included, specifying any metadata columns for either dimension. These should contain information about each row but NOT be required to uniquely identify a row in the ‘colData’ or ‘rowData’ objects. Additional metadata can be attached to a ‘LongTable’ by passing a list to the metadata argument.

### Usage

```
LongTable(
  rowData,
  rowIDs,
  colData,
  colIDs,
  assays,
  metadata = list(),
  keep.rownames = FALSE
)
```

### Arguments

rowData	[‘data.table’, ‘data.frame’, ‘matrix’] A table like object coercible to a ‘data.table’ containing the a unique ‘rowID’ column which is used to key assays, as well as additional row metadata to subset on.
rowIDs	[‘character’, ‘integer’] A vector specifying the names or integer indexes of the row data identifier columns. These columns will be pasted together to make up the row.names of the ‘LongTable’ object.
colData	[‘data.table’, ‘data.frame’, ‘matrix’] A table like object coercible to a ‘data.table’ containing the a unique ‘colID’ column which is used to key assays, as well as additional column metadata to subset on.
colIDs	[‘character’, ‘integer’] A vector specifying the names or integer indexes of the col data identifier columns. These columns will be pasted together to make up the col.names of the ‘LongTable’ object.
assays	A [‘list’] containing one or more objects coercible to a ‘data.table’, and keyed by rowID and colID corresponding to the rowID and colID columns in colData and rowData.
metadata	A [‘list’] of metadata associated with the ‘LongTable’ object being constructed
keep.rownames	[‘logical’ or ‘character’] Logical: whether rownames should be added as a column if coercing to a ‘data.table’, default is FALSE. If TRUE, rownames are added to the column ‘rn’. Character: specify a custom column name to store the rownames in.



**Value**

A [`LongTable`] object containing the data for a treatment response experiment and configured according to the `rowIDs` and `colIDs` arguments.

---

mcc	<i>Compute a Mathews Correlation Coefficient</i>
-----	--

---

**Description**

The function computes a Matthews correlation coefficient for two factors provided to the function. It assumes each factor is a factor of class labels, and the entries are paired in order of the vectors.

**Usage**

```
mcc(x, y, nperm = 1000, nthread = 1, ...)
```

**Arguments**

<code>x, y</code>	factor of the same length with the same number of levels
<code>nperm</code>	numeric number of permutations for significance estimation. If 0, no permutation testing is done
<code>nthread</code>	numeric can parallelize permutation testing using <code>BiocParallels::bplapply</code>
<code>...</code>	list Additional arguments

**Details**

Please note: we recommend you call `set.seed()` before using this function to ensure the reproducibility of your results. Write down the seed number or save it in a script if you intend to use the results in a publication.

**Value**

A list with the MCC as the `$estimate`, and p value as `$p.value`

**Examples**

```
x <- factor(c(1,2,1,2,3,1))
y <- factor(c(2,1,1,1,2,2))
mcc(x,y)
```

---

mDataNames	<i>mDataNames Generic</i>
------------	---------------------------

---

**Description**

A generic for the mDataNames method

**Usage**

```
mDataNames(object, ...)
```

**Arguments**

object	CoreSet object
...	Fallthrough arguments for defining new methods

**Value**

Vector of names of the molecular data types

**Examples**

```
mDataNames(clevelandSmall_cSet)
```

---

mDataNames<-	<i>mDataNames&lt;- Generic</i>
--------------	--------------------------------

---

**Description**

A generic for the mDataNames method

**Usage**

```
mDataNames(object, ...) <- value
```

**Arguments**

object	CoreSet object
...	Fallthrough arguments for defining new methods
value	A character vector with names to be assigned to each list item in the 'molecularProfiles' slot

**Value**

An updated copy of the CoreSet object

**Examples**

```
mDataNames(clevelandSmall_cSet) <- mDataNames(clevelandSmall_cSet)
```

---

merckLongTable	<i>Merck Drug Combination Data LongTable</i>
----------------	--

---

**Description**

This is a LongTable object created from some drug combination data provided to our lab by Merck.

**Usage**

```
data(merckLongTable)
```

**Format**

LongTable object

**References**

TODO:: Include a reference

---

metadata,LongTable-method	<i>Getter method for the metadata slot of a 'LongTable' object</i>
---------------------------	--

---

**Description**

Getter method for the metadata slot of a 'LongTable' object

**Usage**

```
## S4 method for signature 'LongTable'  
metadata(x)
```

**Arguments**

x                   The ['LongTable'] object from which to retrieve the metadata list.

**Value**

'list' The contents of the 'metadata' slot of the 'LongTable' object.

---

```
metadata<- ,LongTable-method
```

*Setter method for the metadata slot of a 'LongTable' object*

---

### Description

Setter method for the metadata slot of a 'LongTable' object

### Usage

```
## S4 replacement method for signature 'LongTable'
metadata(x) <- value
```

### Arguments

x                    ['LongTable'] The LongTable to update  
value                ['list'] A list of new metadata associated with a 'LongTable' object.

### Value

'LongTable' A copy of the 'LongTable' object with the 'value' in the metadata slot.

---

```
molecularProfiles      molecularProfiles Generic
```

---

### Description

Generic for molecularProfiles method

### Usage

```
molecularProfiles(object, mDataType, assay, ...)
```

### Arguments

object                The CoreSet to retrieve molecular profiles from  
mDataType            character The type of molecular data  
assay                 character Name of the desired assay; if excluded defaults to first assay in the SummarizedExperiment for the given mDataType. Use assayNames(molecularProfiles(object, mDataType)) to check which assays are available for a given molecular datatype.  
...                    Fallthrough arguments for defining new methods

### Value

a matrix of data for the given mDataType and assay

### Examples

```
data(clevelandSmall_cSet)
molecularProfiles(clevelandSmall_cSet, "rna")
```

---

molecularProfiles<-    *molecularProfiles<- Generic*

---

**Description**

Generic for molecularProfiles replace method

**Usage**

```
molecularProfiles(object, mDataType, assay) <- value
```

**Arguments**

object	The CoreSet to replace molecular profiles in
mDataType	The type of molecular data to be updated
assay	character Name or index of the assay data to return
value	A matrix with the new profiles

**Value**

Updated CoreSet

**Examples**

```
data(clevelandSmall_cSet)
molecularProfiles(clevelandSmall_cSet, "rna") <- molecularProfiles(clevelandSmall_cSet, "rna")
```

---

molecularProfilesSlot    *molecularProfilesSlot Generic*

---

**Description**

molecularProfilesSlot Generic

**Usage**

```
molecularProfilesSlot(object, ...)
```

**Arguments**

object	A CoreSet from which to return a list of all available SummarizedExperiment objects
...	A list of additional parameters; included to allow adding arguments to methods on this generic

**Value**

A list containing the molecularProfiles from a cSet  
 Generic for molecularProfilesSlot

**Examples**

```
data(clevelandSmall_cSet)
molecularProfilesSlot(clevelandSmall_cSet)
```

---

```
molecularProfilesSlot<-
      molecularProfilesSlot<-
```

---

**Description**

Replace method for the molecular profiles slot of a cSet

**Usage**

```
molecularProfilesSlot(object) <- value
```

**Arguments**

object	A CoreSet object for which values will be replaced
value	A list containing molecular profiles as SummarizedExperiments

**Value**

A copy of the CoreSet with the molecularProfiles slot updated

**Examples**

```
data(clevelandSmall_cSet)
molecularProfilesSlot(clevelandSmall_cSet) <- molecularProfilesSlot(clevelandSmall_cSet)
```

---

name	<i>name Generic</i>
------	---------------------

---

**Description**

A generic for the name method

**Usage**

```
name(object, ...)
```

**Arguments**

object	A CoreSet
...	Fallthrough arguments for defining new methods

**Value**

The name of the CoreSet

**Examples**

```
name(clevelandSmall_cSet)
```

---

name<-

*name<- Generic*


---

**Description**

A generic for the name<- method

**Usage**

```
name(object, ...) <- value
```

**Arguments**

object	A CoreSet object
...	Fallthrough arguments for defining new methods
value	A character string with the name to assign to the cSet

**Value**

The name of the CoreSet

**Examples**

```
name(clevelandSmall_cSet) <- "Cleveland Small"
```

---

pertNumber

*pertNumber Generic*


---

**Description**

A generic for the pertNumber method

**Usage**

```
pertNumber(object, ...)
```

**Arguments**

object	A CoreSet
...	Fallthrough arguments for defining new methods

**Value**

A 3D array with the number of perturbation experiments per drug and cell line, and data type

**Examples**

```
pertNumber(clevelandSmall_cSet)
```

---

```
pertNumber<-          pertNumber<- Generic
```

---

**Description**

A generic for the pertNumber method

**Usage**

```
pertNumber(object) <- value
```

**Arguments**

object	A CoreSet
value	A new 3D array with the number of perturbation experiments per drug and cell line, and data type

**Value**

The updated CoreSet

**Examples**

```
pertNumber(clevelandSmall_cSet) <- pertNumber(clevelandSmall_cSet)
```

---

```
phenoInfo          phenoInfo Generic
```

---

**Description**

Generic for phenoInfo method

**Usage**

```
phenoInfo(object, mDataType, ...)
```

**Arguments**

object	The CoreSet to retrieve rna annotations from
mDataType	the type of molecular data
...	Fallthrough argument for defining new parameters in other S4 methods



**Value**

a data.frame with the experiment info

**Examples**

```
phenoInfo(clevelandSmall_cSet, mDataType="rna")
```

---

phenoInfo<-	<i>phenoInfo&lt;- Generic</i>
-------------	-------------------------------

---

**Description**

Generic for phenoInfo replace method

**Usage**

```
phenoInfo(object, mDataType) <- value
```

**Arguments**

object	The CoreSet to retrieve molecular experiment annotations from
mDataType	the type of molecular data
value	a dataframe with the new experiment annotations

**Value**

The updated CoreSet

**Examples**

```
data(clevelandSmall_cSet)
phenoInfo(clevelandSmall_cSet, mDataType="rna") <- phenoInfo(clevelandSmall_cSet, mDataType="rna")
```

---

reindex	<i>Generic method for resetting indexing in an S4 object</i>
---------	--

---

**Description**

This method allows integer indexes used to maintain referential integrity internal to an S4 object to be reset. This is useful particularly after subsetting an object, as certain indexes may no longer be present in the object data. Reindexing removes gaps integer indexes and ensures that the smallest contiguous integer values are used in an objects indexes.

**Usage**

```
reindex(object, ...)
```

**Arguments**

object            ['S4'] An object to redo indexing for  
 ...              ['pairlist'] Allow definition of new parameters to this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

reindex,LongTable-method

*Redo indexing for a LongTable object to remove any gaps in integer indexes*

---

**Description**

After subsetting a LongTable, it is possible that values of rowKey or colKey could no longer be present in the object. As a result there the indexes will no longer be contiguous integers. This method will calculate a new set of rowKey and colKey values such that integer indexes are the smallest set of contiguous integers possible for the data.

**Usage**

```
## S4 method for signature 'LongTable'
reindex(object)
```

**Arguments**

object            The ['LongTable'] object to recalculate indexes (rowKey and colKey values) for.

**Value**

A copy of the ['LongTable'] with all keys as the smallest set of contiguous integers possible given the current data.

---

rowIDs	<i>Generic to access the row identifiers from</i>
--------	---

---

**Description**

Generic to access the row identifiers from

**Usage**

```
rowIDs(object, ...)
```

**Arguments**

object	[‘S4’] An object to get row id columns from.
...	Allow new arguments to this generic.

**Value**

Depends on the implemented method.

**Examples**

```
print("Generics shouldn't need examples?")
```

---

rowMeta	<i>Generic to access the row identifiers from</i>
---------	---

---

**Description**

Generic to access the row identifiers from

**Usage**

```
rowMeta(object, ...)
```

**Arguments**

object	[‘S4’] An object to get row metadata columns from.
...	Allow new arguments to this generic.

**Value**

Depends on the implemented method.

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityInfo	<i>Generic function to get the annotations for a treatment response experiment from an S4 class</i>
-----------------	---

---

**Description**

Generic function to get the annotations for a treatment response experiment from an S4 class

**Usage**

```
sensitivityInfo(object, ...)
```

**Arguments**

object	An ['S4'] object to get treatment response experiment annotations from.
...	Allow new arguments to be defined for this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityInfo<-	<i>sensitivityInfo&lt;- Generic Method</i>
-------------------	--

---

**Description**

Generic function to get the annotations for a treatment response experiment from an S4 class.

**Usage**

```
sensitivityInfo(object, ...) <- value
```

**Arguments**

object	An ['S4'] object to set treatment response experiment annotations for.
...	Allow new arguments to be defined for this generic.
value	The new treatment response experiment annotations.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityMeasures    *sensitivityMeasures Generic*

---

**Description**

Get the names of the sensitivity summary metrics available in an S4 object.

**Usage**

```
sensitivityMeasures(object, ...)
```

**Arguments**

object	An ['S4'] object to retrieve the names of sensitivity summary measurements for.
...	Fallthrough arguments for defining new methods

**Value**

Depends on the implemented method

**Examples**

```
sensitivityMeasures(clevelandSmall_cSet)
```

---

sensitivityMeasures<-    *sensitivityMeasures<- Generic*

---

**Description**

Set the names of the sensitivity summary metrics available in an S4 object.

**Usage**

```
sensitivityMeasures(object, ...) <- value
```

**Arguments**

object	An ['S4'] object to update.
...	Allow new methods to be defined for this generic.
value	A set of names for sensitivity measures to use to update the object with.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityProfiles    *sensitivityProfiles Generic*

---

**Description**

A generic for sensitivityProfiles getter method

**Usage**

```
sensitivityProfiles(object, ...)
```

**Arguments**

object	The ['S4'] object to retrieve sensitivity profile summaries from.
...	['pairlist'] Allow defining new arguments for this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityProfiles<-    *sensitivityProfiles<- Generic*

---

**Description**

A generic for the sensitivityProfiles replacement method

**Usage**

```
sensitivityProfiles(object, ...) <- value
```

**Arguments**

object	An ['S4'] object to update the sensitivity profile summaries for.
...	Fallthrough arguments for defining new methods
value	An object with the new sensitivity profiles. If a matrix object is passed in, converted to data.frame before assignment

**Value**

Updated CoreSet

---

sensitivityRaw	<i>sensitivityRaw Generic Method</i>
----------------	--------------------------------------

---

**Description**

Generic function to get the raw data array for a treatment response experiment from an S4 class.

**Usage**

```
sensitivityRaw(object, ...)
```

**Arguments**

object	An ['S4'] object to extract the raw sensitivity experiment data from.
...	['pairlist'] Allow new parameters to be defined for this generic.

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensitivityRaw<-	<i>sensitivityRaw&lt;- Generic</i>
------------------	------------------------------------

---

**Description**

Generic function to set the raw data array for a treatment response experiment in an S4 class.

**Usage**

```
sensitivityRaw(object, ...) <- value
```

**Arguments**

object	An ['S4'] object to extract the raw sensitivity data from.
...	['pairlist'] Allow new parameters to be defined for this generic.
value	An object containing dose and viability metrics to update the object with.

**Value**

Depends on the implemented method

---

sensitivitySlot      *sensitivitySlot Generic*

---

**Description**

sensitivitySlot Generic

**Usage**

```
sensitivitySlot(object, ...)
```

**Arguments**

object            A CoreSet to extract the raw sensitivity data from  
 ...                A list to allow new parameters in specific methods

**Value**

A list of the sensitivity slot contents

**Examples**

```
data(clevelandSmall_cSet)
sensitivitySlot(clevelandSmall_cSet)
```

---

sensitivitySlot<-      *sensitivitySlot<- Replacement Generic*

---

**Description**

sensitivitySlot<- Replacement Generic

**Usage**

```
sensitivitySlot(object, ...) <- value
```

**Arguments**

object            A CoreSet to extract the raw sensitivity data from  
 ...                A list to allow new parameters in specific methods  
 value             A list of new sensitivity slot data for the rSet

**Value**

A copy of the CoreSet containing the updated sensitivity slot

**Examples**

```
data(clevelandSmall_cSet)
sensitivitySlot(clevelandSmall_cSet) <- sensitivitySlot(clevelandSmall_cSet)
```



---

sensitivitySlotToLongTable  
*sensitivitySlotToLongTable Generic*

---

**Description**

Convert the sensitivity slot in an object inheriting from a CoreSet from a list to a LongTable.

**Usage**

```
sensitivitySlotToLongTable(object, ...)
```

**Arguments**

object            ['CoreSet'] Object inheriting from CoreSet.  
 ...              Allow new arguments to be defined on this generic.

**Value**

A ['LongTable'] object containing the data in the sensitivity slot.

**Examples**

```
print("Generics shouldn't need examples?")
```

---

sensNumber            *sensNumber Generic*

---

**Description**

A generic for the sensNumber method

**Usage**

```
sensNumber(object, ...)
```

**Arguments**

object            A CoreSet  
 ...              Fallthrough arguments for defining new methods

**Value**

A data.frame with the number of sensitivity experiments per drug and cell line

**Examples**

```
sensNumber(clevelandSmall_cSet)
```

sensNumber<-                    *sensNumber<- Generic*

---

**Description**

A generic for the sensNumber method

**Usage**

```
sensNumber(object) <- value
```

**Arguments**

object	A CoreSet
value	A new data.frame with the number of sensitivity experiments per drug and cell line

**Value**

The updated CoreSet

**Examples**

```
sensNumber(clevelandSmall_cSet) <- sensNumber(clevelandSmall_cSet)
```

---

show,CoreSet-method    *Show a CoreSet*

---

**Description**

Show a CoreSet

**Usage**

```
## S4 method for signature 'CoreSet'  
show(object)
```

**Arguments**

object	CoreSet
--------	---------

**Value**

Prints the CoreSet object to the output stream, and returns invisible NULL.

**Examples**

```
show(clevelandSmall_cSet)
```

---

showSigAnnot	<i>Get the annotations for a 'Signature' class object, as returned by 'drugSensitivitysig' or 'radSensitivitySig' functions available in 'PharmacGx' and 'RadioGx', respectively.</i>
--------------	---

---

### Description

Get the annotations for a 'Signature' class object, as returned by 'drugSensitivitysig' or 'radSensitivitySig' functions available in 'PharmacGx' and 'RadioGx', respectively.

### Usage

```
showSigAnnot(object, ...)
```

### Arguments

object	A 'Signature' class object
...	Allow definition of new arguments to this generic

### Value

NULL Prints the signature annotations to console

### Examples

```
print("Generics shouldn't need examples?")
```

---

subset, LongTable-method

*Subset method for a LongTable object.*

---

### Description

Allows use of the colData and rowData 'data.table' objects to query based on rowID and colID, which is then used to subset all value data.tables stored in the dataList slot. This function is endomorphic, it always returns a LongTable object.

### Usage

```
## S4 method for signature 'LongTable'
subset(x, i, j, assays, reindex = TRUE)
```

**Arguments**

x	[‘LongTable’] The object to subset.
i	[‘character’], [‘numeric’], [‘logical’] or [‘expression’] Character: pass in a character vector of drug names, which will subset the object on all row id columns matching the vector. Numeric or Logical: these select based on the rowKey from the ‘rowData’ method for the ‘LongTable’. Call: Accepts valid query statements to the ‘data.table’ i parameter, this can be used to make complex queries using the ‘data.table’ API for the ‘rowData’ data.table.
j	[‘character’], [‘numeric’], [‘logical’] or [‘expression’] Character: pass in a character vector of drug names, which will subset the object on all drug id columns matching the vector. Numeric or Logical: these select based on the rowID from the ‘rowData’ method for the ‘LongTable’. Call: Accepts valid query statements to the ‘data.table’ i parameter, this can be used to make complex queries using the ‘data.table’ API for the ‘colData’ data.table.
assays	[‘character’, ‘numeric’ or ‘logical’] Optional list of assay names to subset. Can be used to subset the assays list further, returning only the selected items in the new LongTable.
reindex	[‘logical’] Should the col/rowKeys be remapped after subsetting. defaults to TRUE. For chained subsetting you may be able to get performance gains by setting to FALSE and calling reindex() manually after subsetting is finished.

**Value**

‘LongTable’ A new ‘LongTable’ object subset based on the specified parameters.

**Examples**

```
# Character
subset(merckLongTable, 'CAOV3', 'ABT-888')
# Numeric
subset(merckLongTable, 1, c(1, 2))
# Logical
subset(merckLongTable, rowData(merckLongTable)$cell_line1 == 'A2058')
# Call
subset(merckLongTable, cell_line1 == 'A2058',
       drug1 == 'Dasatinib' & drug2 != '5-FU')
```

---

summarizeMolecularProfiles

*Summarize molecular profile data such that there is a single entry for each cell line/treatment combination*

---

**Description**

Summarize molecular profile data such that there is a single entry for each cell line/treatment combination

**Usage**

```
summarizeMolecularProfiles(object, ...)
```

**Arguments**

object            An ['S4'] object to summarize the molecular profiles for.  
...                Allow definition of new arguments to this generic

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

summarizeSensitivityProfiles

*Summarize across replicates for a sensitivity dose-response experiment*

---

**Description**

Summarize across replicates for a sensitivity dose-response experiment

**Usage**

```
summarizeSensitivityProfiles(object, ...)
```

**Arguments**

object            An ['S4'] object to summarize sensitivity profiles for.  
...                Allow definition of new arguments to this generic

**Value**

Depends on the implemented method

**Examples**

```
print("Generics shouldn't need examples?")
```

---

```
[,LongTable,ANY,ANY,ANY-method
  [ LongTable Method
```

---

## Description

Single bracket subsetting for a LongTable object. See subset for more details.

## Usage

```
## S4 method for signature 'LongTable,ANY,ANY,ANY'
x[i, j, assays, ..., drop = FALSE]
```

## Arguments

x	[‘LongTable’] The object to subset.
i	[‘character’], [‘numeric’], [‘logical’] or [‘call’] Character: pass in a character vector of drug names, which will subset the object on all row id columns matching the vector. This parameter also supports valid R regex query strings which will match on the colnames of ‘x’. For convenience, * is converted to .* automatically. Colon can be to denote a specific part of the colnames string to query. Numeric or Logical: these select based on the rowKey from the ‘rowData’ method for the ‘LongTable’. Call: Accepts valid query statements to the ‘data.table’ i parameter as a call object. We have provided the function .() to conveniently convert raw R statements into a call for use in this function.
j	[‘character’], [‘numeric’], [‘logical’] or [‘call’] Character: pass in a character vector of drug names, which will subset the object on all drug id columns matching the vector. This parameter also supports regex queries. Colon can be to denote a specific part of the colnames string to query. Numeric or Logical: these select based on the rowID from the ‘rowData’ method for the ‘LongTable’. Call: Accepts valid query statements to the ‘data.table’ i parameter as a call object. We have provided the function .() to conveniently convert raw R statements into a call for use in this function.
assays	[‘character’] Names of assays which should be kept in the ‘LongTable’ after subsetting.
...	Included to ensure drop can only be set by name.
drop	[‘logical’] Included for compatibility with the ‘[]’ primitive, it defaults to FALSE and changing it does nothing.

## Details

This function is endomorphic, it always returns a LongTable object.

## Value

A [‘LongTable’] containing only the data specified in the function parameters.

**Examples**

```
# Character
merckLongTable['CAOV3', 'ABT-888']
# Numeric
merckLongTable[1, c(1, 2)]
# Logical
merckLongTable[rowData(merckLongTable)$cell_line1 == 'A2058', ]
# Call
merckLongTable[(cell_line1 == 'A2058'),
               .(drug1 == 'Dasatinib' & drug2 != '5-FU')]
```

---

\$,LongTable-method      *Select an assay from a LongTable object*

---

**Description**

Select an assay from a LongTable object

**Usage**

```
## S4 method for signature 'LongTable'
x$name
```

**Arguments**

x	A ['LongTable'] object to retrieve an assay from
name	['character'] The name of the assay to get.

**Value**

'data.frame' The assay object.

**Examples**

```
merckLongTable$viability
```

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